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WELCOME TO THE U.S. PATENT TEXT FILE

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2157 INFLUENZA L1

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Recombinant negative strand RNA virus

L2: 1 of 13 US PAT NO:

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TITLE:

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## ABSTRACT:

Recombinant negative strand virus RNA templates which may be used to express heterologous gene products and/or to construct chimeric viruses are described. \*\*Influenza\*\* viral polymerase, which was prepared depleted of viral RNA, was used to copy small RNA templates prepared from plasmid-encoded sequences. Template constructions containing only the 3' end of genomic RNA were shown to be efficiently copied, indicative that the promoter lay solely within the 15 nucleotide 3' terminus. Sequences not specific for the \*\*influenza\*\* vital termini were not copied, and, surprisingly, RNAs containing termini identical to those from plus sense cRNA were copied at low levels. The specificity for recognition of the virus-sense promoter was further defined by site-specific mutagenesis. It was also found that increased levels of vital protein were required in order to catalyze both the cap-endonuclease primed and primer-free RNA synthesis from these model templates as well as from genomic length RNAs. This indicated that this reconstituted system had catalytic properties very smilar to those of native viral RNPs. High levels of expression of a heterologous gene was obtained using the constructs and methods described.

**5,549,896 [IMAGE AVAILABLE]** L2: 2 of 13 **US PAT NO:** Hepatitis a virus strain, method for the isolation of new TITLE: hepatitis a virus strains and hepatitis a vaccines

## ABSTRACT:

The invention relates to hepatitis A viruses (HAVs) having a serotype displaying the immunological characteristics of the HAV strain RG-SB XA112 (CNCM I-1080). In particular, the invention relates to the new hepatitis A virus strain RG-SB XA112 (CNCM I-1080). The invention also relates to structural components of said HAVs. Furthermore, the invention relates to processes for the isolation of said HAVs. The HAVs of the present invention and the structural components thereof can be used for the production of vaccines and diagnostic compositions. Finally, the

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/codon\_start=1 /note="polymerase basic 2; NCBI gi: 324982" organism="Influenza virus type A"

DVIHEVVEPNEVGARILISESQLTITKEXKEELQDCKISPLMVAYHLERELVRKTRFL PVAGGTSSVYIEVLHLTQGTCMEQMYTP GEEVRINDIVDQSLITARNIVRRAAVSADP LASLLEMCHSTQIGGTRMVDILRQNP TEEQAVEICKAAMGLRISSSF STGGTTEKRTS GSSVKREEEVLTGNLQTLK IRVHEGYEEFTMVGKRATAILRKATRRLIQLIVSGRDEQ SIAEAIIVAMVESQEDCHIKANGGLRFVNRAMQBLNPMHQLLHHFQKDAKVLFQNWG EHIDNVMGMIGVLPDMTP STEMSKRGVRVSKMGVDEYSSAERVVVSIDRFLRVEDQR PPKQSRMQFSSLTVNVRGSGMRILVRGNSPIFNYNKTTKRLTILGKDAGTLTEDPDEG TSGYESAVLRGFLLLGKEDRRYGPALSINELSNLAKGEXANVLIGQGDVVLVMKRKRN SSILTDSQTATKRIRMAIN" GNVLLSPEEVSETQGTEKLTITYSSSMMHEINGPESVLVNTYQMITRNMETYKLQMSQ NPTMLYNKMEFEPFQSLVPKAIRGQYSGFVRTLFQQMRDVLGTFDTTQIIKLLPFAAA GPMTSTVHYPKIYKTYFEKVERLKHGTFGPVHFRNQVKIRRRVDINPGHADLSAKEAQ LRMKWMMAMKYP I TADKR I TEMI PERNEQGQTLWSKWSDAGSDRVMVSP LAVTWWNRN translation="MERIKELRNIMSQSRTREILTKTTVDHMAIIKKYTSGRQEKNPS/ /db\_xref="PID:g324982"

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mutation mutation

ORIGIN Query Match 99.1%; Best Local Similarity 76.6%; 

닭 Matches 1 agcgaaagcaggtcaattatattcaatatggaaagaataaaagaactacggaatctgatg 1793; Conservative Score 2321; DB 71; Pred. No. 0.00e+00; Mismatches <u>1</u>0; Indels 0; Gaps 0; 69

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Score 1021; DB 3; Length 1027;

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Vaccine; cytotoxic T lymphocyte; CTL; matrix protein; 25-AUG-1993 Influenza MI gene. anti-viral agent; 88. Influenza A virus.

/\*tag= /product= Influenza\_A\_virus\_Matrix\_protein ω 1..759

Location/Qualifiers

12-MAY-1993. EP-541335-A.,

04-NOV-1992; 310067. 08-NOV-1991; US-792507.

Montgomery.DL, Oliff AA, WPI; 93-154266/19. (MERI ) MERCK & CO INC. Donnelly JJ, Friedman A, Hawe LA, Liu MA, Shi X, Ulmer J;

Marshall

.P-PSDB; R36804. useful as vaccines against viral infections, tumours and Recombinant DNA encoding bacterial toxin-antigen conjugates

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and II coding regions of Pseudomonas exotoxin into pBluescript II SK restricted with HincII and SacII). The PF-derived portion of the hybrid protein allows internalisation of the protein by an The MI gene (encoding influenza A virus matrix protein) was amplified from pApr701 with primers which added a SacII site adjacent to MI codon number 2 and a SacI site 3' of the MI SacII and SacI. (BS-PE is constructed by inserting a 1.3kb NruI/SacII fragment of plasmid pVC45-DF+T containing the domain I termination codon (Q41705 and Q41706, respectively). The amplified fragment was then subcloned into BS-PE which had been restricted by Example 1; Page 16-17; 81pp; English parasites an antiquent segment (i.e. the Influenza A virus matrix protein) is presented on the cell surface where it elicits an immune response. Sequence antigen-presenting cell. The hybrid protein is then processed and 759 BP; 218 A;

Best Local Similarity 74.6%; Query Match Matches 566; Conservative 164; Mismatches 68.3%; Score 701; DB 7; 74.6%; Pred. No. 0.00e+00; DB 7; Length 759; 29; Indels <u>.</u> Gaps 0

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	Cox, N.J., Kitame, F., Kendal, A.P., Maassab, H.F. and Naeve, C.	AUTHORS
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241 aagcacagatttgaaataatagagggaagagatcgcacaatggcctggacagiagcadac	Qy 181 UUCAUCAAUGAGCAAGGCGAGUCAAUAAUAGUAGAGGCUGAGGAGGCGAGGGCGAGGGAGG		ру 121 амсьялилисскаесьалилиссастисственности объести при примененности примененности примененности примененности при примененности примененност	Db 121 aacaaatttgcagcattagcactcacttggaagtatgcttcatgtattcagattttcat 180		Db 61 attgtcgagcttgddgaaaagcaatgaaagagtatggaagaggatctgaaaatcdgaaaca 120		agcgaaagcaggtactgaftbgaaatggaagattttgtgcgacaatgcttcaatccgatg 60	Query Match 99.6%; Score 2223; DB 71; Length 2233; Best Local Similarity 75.7%; Pred. No. 0.00e+00; Matches 1690; Conservative 538; Mismatches 5; Indels 0; Caps 0	BASE COUNT 746 a 419 c 526 g 542 c c c c c c c c c c c c c c c c c c c	ion 216721 /note="ti	mutation 1861 /note="a in wild type; g in mutant".	SHLRINTDVVNFVSMEFSLTDPRLEPHKWEKYCVLEIGDMLLRSAIGQVSRPMFLYVR TNGTSKIKMKWGMEMRRCLLQSIQQIESMIEAESSVKEKDMTKEFFKQNKSETWPIGES PKGVEEGSIGKVCRTLLAKSVFNSLYASPQLEGFSAESRKLLLVVQALRDNLEPGTFD LGGLYEAIEECLINDPWVLLNASWFNSFLTHALR."	ILSWKQVIAEIDE EXEKT PRYKNMKKTSQIKWALGENMAPEKVDEDDCRDVSDIKQ ILSWKQVIAEIDE IEXEEKT PRYKNMKKTSQIKWALGENMAPEKVDEDDCRDVSDIKQ YDSDEPELMSILSSWIQNEENKACELIDSIWIELDEIGEDVAPIEHIASMRRNYETÄEV SHCRAYEY,MKGVYINTALLNASCAAMDDEQLIPMISKCRTKKEGRRKTNLYGFIIKGR	YTLDEESRARIKTRLFTIRQEMASRGLMDSFHQSERGEETIEERFEITGTMRRLADQS LPPNESGLENFRAYVDGFEPNGYIEGKLSQMSKEVNAKIEPFLKTTPRPIRLPDGPPC GOD KKELI MONIKLSTENDSHRGEGTPLVDAIKGMBTEFGMKEPYVVKPHEKGINPNY	/db_xret="p.ii:q2x4yxo" /tr=mblation="#EDFYRQCFNPHIVELAEKAHKEYGEDIKIETNKEAAICTHIEV /tr=mblation="#EDFYRQCFNPHIVELAEKAHKEYGEDIKIETNKEAAICTHIEV cFMYSDFHFINEQGESIIVELDPNALLKHRFEIIEGRRRTHAMTVVNSICNTTGAEK cFMYSDFHFINEQGESIIVELGVHTRRFVHIYYLEKANKIKSEKTHIHIESFTGEEMATKAD	/not /co	mutation 20 /note="t in wild type; c in mutant" ()  CDS 252175		NCBI gi: 324925 Location/Qualifiers	MEDLINE 89073/59  COMMENT Draft entry and computer-readable sequence [Virology 167. 559-567]  (1989)] kindly submitted by  N.J.Cox, 11-APR-1989.	attenuated influenza vaccine strain, A/Ann Arbor/6/60(HZNZ)	The second of th	, Negative strand TNA viruses; Influenza A viruses.	32)142 US-08-573-569-11.rge 3	
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				1081 aa	1021-AA	aa	,1 	_ 8;	901 GA	. · 8		9	- 14 - 12 - 12 - 12 - 12 - 12 - 12 - 12 - 12	gt g	agg	601 cag	. AC =	acc	6AA	GAA)	361> AAGG	361 aagg	l agta 	AAGC	8	